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(54) Title: METHOD FOR ANALYSIS OF METHYLATED NUCLEIC ACIDS

(57) Abstract: A method is disclosed providing analysis of the degree of methylation within nucleic acid samples, including the degree of methylation within CpG islands. After bisulfite treatment of a nucleic acid sample to convert cytosines to uracils, multiple species of paired oligonucleotide primers and optionally a methylation insensitive reference primer pair are used to amplify target sequences within the sample by methylation specific PCR. Amplification of multiple primer pairs is combined with the use of a real time PCR. Amplificates of primer pairs are detected and quantified by comparison, thus allowing for a detailed, more specific, and quantifiable analysis of the methylation status within a complex CpG methylation pattern of a nucleic acid sample. Primer pairs and a kit are also disclosed.